

					Atty Docke	t No.	Serial No.
					M-9023-1 V	JS	09/495,668
TNTPO	RMATIC	N DISCLOSURE	STATEMENT BY	APPLICANT	Applicant(s)	
			eets if necessary)		Selifonov e	t al.	
<u> </u>				Filing Date		Group	
					February 1	L, 2000	1643
			U.S. P	atent Documents			
Examiner Initial		Document Number	Date	Name	Class	Subclass	Filing Date If Appropriate
- Uh	1.	5,512,463	*04-30-1996	Stemmer	435		6/1/94
	2.	5,514,588	05-07-1996	Varadaraj et al.	.435		12/13/94
/- -	3.	5,605,793	02-25-1997	Stemmer	435		2/17/94
	4.	5,763,239	06-09-1998	Short et al.	435		6/18/96
	5.	5,789,228	08-04-1998	Lam et al.	435		5/22/96
	6.	5,811,238	*09-22-1998	Stemmer et al.	435		11/30/95
	7.	5,814,473	09-29-1998	Warren et al.	435		2/9/96
	8.	5,824,469	10-20-1998	Horwitz et al.	435		9/30/94
	9.	5,830,696	11-03-1998	Short	435		12/5/96
	10.	5,830,721	*11-03-1198	Stemmer et al.	435		3/4/96
	11.	5,834,252	11-10-1998	Stemmer et al.	433		4/18/95
	12.	5,837,458	*11-17-1998	Minshull et al.	435		5/20/96
	13.	5,866,363	02-02-1999	Pieczenik	435		2/28/91
	14.	5,876,997	03-02-1999	Kretz	435		- 8/13/97
	15.	5,925,749	*07-20-1999	Mathur et al.	536		4/24/98
	16.	5,928,905	07-27-1999	Stemmer et al.	435		7/3/96
	17.	5,939,250	*08-17-1999	Short	435		5/22/96
	18.	5,939,300	08-17-1999	Robertson et al.	435		7/3/96
	19.	5,942,430	08-24-1999	Robertson et al.	435		2/16/96
	20.	5,948,666	09-07-1999	Callen et al.	435		8/6/97
	21.	5,958,672	09-28-1999	Short	435		6/3/96
	22.	5,958,751	09-28-1999	Murphy et al.	435		3/8/96
	23.	5,962,258	10-05-1999	Mathur et al.	435		8/23/95
	24.	5,962,283	10-05-1999	Warren et al.	435		5/8/96
	25.	5,965,408	10-12-1999	Short	435	-	7/9/96
	26.	5,985,646	11-16-1999	Murphy et al.	435		4/24/98
	27.	6,001,574	*12-14-1999	Short et al.	435		3/4/98
	28.	6,004,788	*12-21-1999	Short	435		7/18/95
- 	29.	6,030,779	*02-29-2000	Short	435		10/6/97

N	30.	6,054,267	*04-25-2000	Short	435		8/2/9	•
1			Foreign	Patent Documents				
								islatio
		Document	Date	Country	Class	Subclass	Yes	N
16	31.	97/07205	02-27-1997	wo				_
	32.	97/20078	06-05-1997	wo				<u> </u>
	33.	97/25410	07-17-1997	wo				+
	34.	97/35957	10-02-1997	wo				+
	35.	97/35966	10-02-1997	wo				_
_	36.	97/44361	11-27-1997	WO				_
	37.	97/48416	12-24-1997	wo				_
	38.	97/48717	12-24-1997	wo				
\dashv	39.	97/48794	12-24-1997	wo				
+	40.	98/00526	01-08-1998	wo				
	41.	98/01581	01-15-1998	wo				
_ -	42.	98/13485	04-02-1998	wo				<u> </u>
	43.	98/13487	04-02-1998	wo		<u></u>		
-	44.	98/24799	06-11-1998	wo				\perp
_	45.	98/27230	06-25-1998	wo				_
	46.	98/28416	07-02-1998	wo				
-	47.	98/31387	07-23-1998	wo				
	48.	98/36080	08-20-1998	wo				
_	49.	98/41622	09-24-1998	wo				\bot
-	50.	98/41623	09-24-1998	wo				
-	51.	98/41653	09-24-1998	wo				
 	52.	98/42832	10-01-1998	wo	-			
	53.	98/48034	10-29-1998	wo	-			
_	54.	98/58085	12-23-1998	wo	_			
	55.	99/07837	02-19-1999	wo	-			
+	56.	99/08539	02-25-1999	wo	-			
	57.	99/10472	03-04-1999	wo				
+	58.	99/10539	03-04-1999	wo				
	59.	99/19518	04-22-1999	WO · · · ·				
+	60.	0911396A2	04-28-1999	EP				
	61.	99/21979	05-06-1999	wo		7		
+	62.	0911396A3	05-06-1999	EP				\perp
1/	63.	99/23107	05-14-1999	₩o	-			

APR. 30. 2003 12:28PM

,						T	· ·
i M	64.	99/23236	05-14-1999	wo			
	65.	0934999A1	08-11-1999	EP			
	66.	99/41368	08-19-1999	WO			
_	67.	99/41369	08-19-1999	wo	-		
+-	68.	99/41383	08-19-1999	WO			
	69.	99/41402	08-19-1999	WO			
-1	70.	99/45154	09-10-1999	wo			
-	71.	99/57128	11-11-1999	wo			· _
	72.	99/65927	12-23-1999	WO			
	73.	00/37684	06-29-2000	WO			
V	1,3.	OTHER	ART (Including Aut	nor, Title, Date, Per	tinent Pages,	Etc.)	
	74		Automated Design of				in Science 199
1	74.	pages 1333-133	6.	uio o di giori			
/		1				alastian " Saia	
	75.	Dahiyat et al., 3, 1997, pages8	<u>De Novo Protein Des</u> 2-87.	en: Fully Automate	a Sequence S	erection, sere	. ————
	76.	Dahiyat et al., "De Novo Protein Design: Towards Fully Automated Sequence Selection," J. Mol. Biol. 1997 273, pages 789-796.					
	77.	Dahiyat et al., "Probing the Role of Packing Specificity in Protein Design," Proc. Natl. Acad. September 1997, vol. 94, pages 10172-10177.					1. Acad. Sci. U
	78.	Design," Struct	iyo, " <u>Branch-and-Terr</u> ure, September 1999,	pages 1089-1098	Judenske er		
	79.	Gordon et al., " 509-513.	Energy Functions for	Protein Design," Cu	ment Opinion	i in Structural I	Biology, 1999,
	80.	Based on the D	iyo, " <u>Radical Perform</u> ead-End Elimination ?	Theorem," Journal o	f Computatio	nal Chemistry,	. 1998, VOI. 19,
	81.	Haney et al., "Structural Basis for Thermostability and Identification of Potential Active Site Resident Adenylate Kinases From the Archaeal Genus Methanococcus," Proteins: Structure, Function, and Genetics, 1997, pages 117-130.				unction, and	
	<u> </u>	82. Malakauskas and Mayo, 'Design, Structure and Stability of a Hyperthermophilic P Natural Structural Biology, June 1998, vol. 5 number 6, pages 470-475.					
	82.	Malakauskas a Natural Structu	nd Mayo, <u>"Design, Str</u> ral Biology, June 1999	3, vol. 5 number 6, p	nages 470-475). 	
	82.	Malakauskas an Natural Structu Pollock et al., *	nd Mayo, "Design, Str	8, vol. 5 number 6, pesidues: Maximum	nages 470-475). 	
		Malakauskas an Natural Structu Pollock et al., ' Structure," J. M	nd Mayo, " <u>Design, Str</u> ral Biology, June 1999 	8, vol. 5 number 6, p esidues: Maximum 187-198.	Likelihood Id	lentification an	d Relationship

in	86	Street and Mayo, "Pairwise Calculation of Protein Solvent-Accessible Surface Areas," Folding & Design, June 3, 1998, pages 253-258.
	87.	Strop and Mayo, "Rubredoxin Variant Folds without Iron," American Chemical Society, March 24, 1999, vol. 121, number 11, pages 2341-2345.
	88.	Wollenberg and Atchley. "Separation of Phylogenetic and Functional Associations in Biological Sequences by Using the Parametric Bootstrap," PNAS, March 28, 2000, vol. 97, pages 3288-3291.
	89	Stemmer, "DNA Shuffling by Random Fragmentation and Reassembly: In Vitro Recombination for Molecular Evolution," Proc. Natl. Acad. Sci. USA, October 1994, vol. 91, pages 10747-10751.
	90.	Venkatasubramanian et al., "Evolutionary Design of Molecules with Desired Properties Using the Genetic Algorithm," J. Chem. Inf. Comput. Sci., 1995, vol. 35pages 188-195.
	91.	Whipple et al., "Application of Genetic Algorithms to Combinatorial Synthesis: A Computational Approach to Lead Identification and Lead Optimization," J. AM. Chem. Soc., 1996, vol. 118, pages 1669-
	92.	1676. Harayama, Shigeaki, "Artificial Evolution by DNA Shuffling," Tibtech, February 1998, vol. 16, pages pages 16-19 and pages 80-82.
	93.	Zhang, Ching, "A Genetic Algorithm for Molecular Sequence Comparison," Proceedings of the International Conference on Systems, Man, and Cybernetics, 1994, pages 1926-1931.
	⊲94.	Stemmer et al., "Single-Step assembly of a Gene and Entire Plasmid from Large Numbers of Oligodeoxyribonucleotides," Gene, 1995, vol. 164, pages 49-53.
Examiner *	The	Date Considered 5-4-03
	: Initial i	if reference considered, whether or not citation is in conformance with MPEP 609; Draw line through mance and not considered. Include copy of this form with your communication to applicant.

Serial No.: 09/495,668

Form 1449 (Modified)	Atty Docket No. MXGNP002X1	Application No.: 09/495,668
Information Disclosure Statement By Applicant	Applicant: Selifonov et al.	
(Use Several Sheets if Necessary)	Filing Date February 1, 2000	Group 1631

ILS. Patent Documents

		<u> </u>	Ua). I att			1 = -	1
Examiner Initial	No.	Patent No.	Date	Patentee	Class	Sub- class	Filing Date
		6,125,381	9/26/00	Toh			<u> </u>
	A2	6,403,312	6/11/02	Bassil, et al			
	A3					<u> </u>	

Foreign Patent or Published Foreign Patent Application

Examiner		Document	Publication	Country or		Sub-		slation
Initial	No.	No.	Date	Patent Office	Class	class	Yes	No
	B1	WO00/47612	8/ 1 7/00	WIPO				
	B2	WO01/61344	8/23(01	WIPO				<u> </u>
	B3	WO00/42559	7/2/00	WIPO				
	B4	WO01/75767	10/11/01	WIPO		<u> </u>		

Other Documents

		Other Mocuments
Examiner Initial	No.	Author, Title, Date, Place (e.g. Journal) of Publication
	Cl	Young et al., "Characterization of Receptor Binding Determinants of Granulocyte Colony Stimulating Factor," Protein Science 6:1228-1236, 1997
	C2	Dahiyat and Mayo, "Protein Design Automation," Protein Science, 5:895-903, (1996)
	C3	Su et al., "Coupling Backbone Flexibility and Amino Acid Sequence Selection in Protein Design," Protein Science, 6:1701-1707, (1997)
	C4	Voigt et al., "Computationally Focusing the Directed Evolution of Proteins," Journal of Cellular Biochemistry Supplement, 37:58-63 (2001)
	C5	Hellberg et al., "Minimum Analogue Peptide Sets (MAPS) for quantitative Structure-Activity Relationships," Int. J. Peptide Protein Res. 37:414-427 (1991)

pot

Pg. 1 of 3

Form 1449 (Modified)	Atty Docket No. MXGNP002X1	Application No.: 09/495,668
Information Disclosure Statement By Applicant	Applicant Selifonov et al.	
(Use Several Sheets if Necessary)	Filing Date February 1, 2000	Group 1631

	·	
	C6	Martin van Heel, "A New Family of Powerful Multivariates Statistical
	_	Sequence Analysis Techniques." J. Mol. Biol, 220:877-887 (1991)
	C7	Goldman et al "Festimating Protein Function From Combinatorial Sequence
,)	Data Using Decision Algorithms and Neural Networks," Drug Dev. Research
		33:125-132 (1994)
	C8	Gustafsson et al., "Exploration of Sequence Space for Protein Engineering," J.
		Mol. Recognit 14:308-314 (2001)
	C9	Miyazawa et al., "Residue-Residue Potentials with a Favorable Contact Pair
	0/	Texm and an Unfavorable High Packing Density Term, for Simulation and
		Threading," J. Mol. Biol., 256:623-644 (1996)
	C10	
• •	010	Using a Simplified Model," Proteins: Structure, Function, and Genetics,
		31:299-308 (1998)
	C11	
	~~~	Engergies Based on an Equilibrium Mixture Approximation of Residues,"
	Į	Proteins: Structure, Function, and Genetics, 34:49-68 (1999)
	C12	Miyazawa et al., "An Empirical Energy Potential With a References State for
		Protein Fold and Sequence Recognition," Proteins: Structure, Function, and
		Genetics, 36:357-369 (1999)
	C13	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
		Vol. 98, No. 6, 3226-3231 (2001)
-	C14	Lehman et al., "Engineering Proteins for Thermostability: the Use of
		Sequence Alignments Versus Rational Design and Directed Evolution,"
		Current Opinion in Biotechnology, 18:371-375 (2001)
	C15	
		Biometrics 50, 653-664, (1994)
	C16	H.W. Hellinga, "Rational Protein Design: Combining Theory and
		Experiment," Proc. Natl. Acad. Sci. USA, Vol. 94, pp. 10015-10017, (1997)
	C17	
		(1997)

NOT Considered

Pg. 2 of 3

## BEST AVAILABLE COPY

Form 1449 (Modified)	Atty Docket No. MXGNP002X1	Application No.: 09/495,668
Information Disclosure Statement By Applicant	Applicant: Selifonov et al. Filing Date	Group
(Use Several Sheets if Necessary)	February 1, 2000	1631

		·		
		Jonsson, et al, "Quaintitative Sequence-Activity Modeils (QSAM)- Tool For Sequence Design", Nuclear Acid Research Vol. 21, No. 3, pp. 733-739 (1993)		
		Sjostrom, et al, "Signal Reptide Amino Acid Sequences In Escheruchua coli Contain Information Related To Final Protein Localization. A Multivariate Data Analysis". The CMBO Journal vol. 6, no. 3, pp 823-831, (1987)		
	C20	Patel, et al, "Patenting Computer-Designed Peptides", Journal Of Computer-Acid Molecular Design 12 pp543-556, (1998)		
	C21			
	C22	Mee, et al, "Design of Active Analogues of a 15-Residue Peptide Using D-Optimal Design QSAR and a Combinatorial Search Algorithm", J Peptide Res. 49, pp. 89-102, (1997)		
	C23	Bogarad, et al, "A Hierarchical Approach to Protein Molecular Evolution", Proc. Natl. Acad. Sci. USA, Vol. 96, pp. 2597-2595, March 1999		
	C24	Darius, et al, "Simulated Molecular Evolution" Or Computer-Generated Artifacts?", Biophysical Journal, Vol. 67, pp. 2120-2122, November 1994		
Examiner	<u></u>	Date Considered		

Examiner: Initial citation considered. Draw line through citation if not in conformance and not considered. Include copy of this form with next communication to applicant.

Not considered

Pg. 3 of 3